



APPENDIX A

SEQ ID NO:4 vs. AA422178

	10	20	30	40	50	60
	*	*	*	*	*	*
SEQ ID NO:4	GGAACGAGGG	AAAATCTGCC	TTCTCACCAT	GAGGCTTCTA	GTCCTTTCCA	GCCTGCTCTG
	CCTTGCTCCC	TTTGTAGACGG	AAGAGTGGTA	CTCCGAAGAT	CAGGAAAGGT	CGGACGAGAC
AA422178		ATCTGCC	TTCTCACCAT	GAGGCTTCTA	GTCCTTTCCA	GCCTGCTCTG>
SEQ ID NO:4		ATCTGCC	TTCTCACCAT	GAGGCTTCTA	GTCCTTTCCA	GCCTGCTCTG

	70	80	90	100	110	120
	*	*	*	*	*	*
SEQ ID NO:4	TATCCTGCTT	CTCTGCTTCT	CCATCTTCTC	CACAGAAGGG	AAGAGGCGTC	CTGCCAAGGC
	ATAGGACGAA	GAGACGAAGA	GGTAGAAGAG	GTGTCTTCCC	TTCTCCGCAG	GACGGTTCGG
AA422178	50	60	70	80	90	100
	TATCCTGCTT	CTCTGCTTCT	CCATCTTCTC	CACAGAAGGG	AAGAGGCGTC	CTGCCAAGGC>
SEQ ID NO:4	TATCCTGCTT	CTCTGCTTCT	CCATCTTCTC	CACAGAAGGG	AAGAGGCGTC	CTGCCAAGGC

	130	140	150	160	170	180
	*	*	*	*	*	*
SEQ ID NO:4	CTGGTCAGGC	AGGAGAACCA	GGCTCTGCTG	CCACCGAGTC	CCTAGCCCCA	ACTCAACAAA
	GACCACTCCG	TCCTCTTGGT	CCGAGACGAC	GGTGGCTCAG	GGATCGGGGT	TGAGTTGTTT
AA422178	120	130	140	150	160	170
	CTGGTCAGGC	AGGAGAACCA	GGCTCTGCTG	CCACCGAGTC	CCTAGCCCCA	ACTCAACAAA>
SEQ ID NO:4	CTGGTCAGGC	AGGAGAACCA	GGCTCTGCTG	CCACCGAGTC	CCTAGCCCCA	ACTCAACAAA

	190	200	210	220	230	240
	*	*	*	*	*	*
SEQ ID NO:4	CCTGAAAGGA	CATCATGTGA	GGCTCTGTAA	ACCATGCAAG	CTTGAGCCAG	AGCCCCGCCT
	GGACTTTCCT	GTAGTACACT	CCGAGACATT	TGGTACGTTC	GAACTCGGTC	TCGGGGCGGA
AA422178	180	190	200	210	220	230
	CCTGAAAGGA	CATCATGTGA	GGCTCTGTAA	ACCATGCAAG	CTTGAGCCAG	AGCCCCGCCT>
SEQ ID NO:4	CCTGAAAGGA	CATCATGTGA	GGCTCTGTAA	ACCATGCAAG	CTTGAGCCAG	AGCCCCGCCT

	250	260	270	280	290	300
	*	*	*	*	*	*
SEQ ID NO:4	TTGGGTGGTG	CCTGGGGCAC	TCCCACAGGT	GTAGCACTCC	CAAAGCAAGA	CTCCAGACAG
	AACCCACCAC	GGACCCCGTG	AGGGTGTCCA	CATCGTGAGG	GTTTCGTCTC	GAGGTCTGTC
AA422178	240	250	260	270	280	290
	TTGGGTGGTG	CCTGGGGCAC	TCCCACAGGT	GTAGCACTCC	CAAAGCAAGA	CTCCAGACAG>
SEQ ID NO:4	TTGGGTGGTG	CCTGGGGCAC	TCCCACAGGT	GTAGCACTCC	CAAAGCAAGA	CTCCAGACAG

	310	320	330	340	350	360
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	CGGAGAACCT	CATGCCTGGC	ACCTGAGGTA	CCCAGCAGCC	TCCTGTCTCC	CCTTTTCAGCC
	GCCTCTTGGA	GTACGGACCG	TGGACTCCAT	GGGTCGTCGG	AGGACAGAGG	GGAAAGTCGG
AA422178	290 CGGAGAACCT	300 CATGCCTGGC	310 ACCTGAGGTA	320 CCCAGCAGCC	330 TCCTGTCTCC	340 CCTTTTCAGCC>
SEQ ID NO:4	CGGAGAACCT	CATGCCTGGC	ACCTGAGGTA	CCCAGCAGCC	TCCTGTCTCC	CCTTTTCAGCC

	370	380	390	400	410	420
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	TTCACAGCAG	TGAGCTGCAA	TGTTGGAGGG	CTTCATCTCG	GGCTGCAAGG	ACCCTGGGAA
	AAGTGTCGTC	ACTCGACGTT	ACAACCTCCC	GAAGTAGAGC	CCGACGTTCC	TGGGACCCCT
AA422178	350 TTCACAGCAG	360 TGAGCTGCAA	370 TGTTGGAGGG	380 CTTCATCTCG	390 GGCTGCAAGG	400 ACCCTGGGAA>
SEQ ID NO:4	TTCACAGCAG	TGAGCTGCAA	TGTTGGAGGG	CTTCATCTCG	GGCTGCAAGG	ACCCTGGGAA

	430	440	450	460	470	480
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	AGTTCCAGAA	CTCCACGTCC	TTGTCTCAAT	TGTGCCATCA	ACTTTCAGAG	CTATCATGAG
	TCAAGGTCTT	GAGGTGCAGG	AACAGAGTTA	ACACGGTAGT	TGAAAGTCTC	GATAGTACTC
AA422178	410 AGTTCCAGAA	420 CTCCACGTCC	430 TTGTCTCAAT	440 TGTGCCATCA	450 ACTTTCAGAG	460 CTATCATGAG>
SEQ ID NO:4	AGTTCCAGAA	CTCCACGTCC	TTGTCTCAAT	TGTGCCATCA	ACTTTCAGAG	CTATCATGAG

	490	500	510	520	530	540
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	CCAACCTCAC	CCCACAGGGC	CTCAGTCGCC	ACCATGTGGG	CCTCTCCAGT	GCAAACCACC
	GGTTGGAGTG	GGGTGTCCCG	GAGTCAGCGG	TGGTACACCC	GGAGAGGTCA	CGTTTGGTGG
AA422178	470 CCAACCTCAC	480 CCCACAGGGC	490 CTCAGTCGCC	500 ACCATGT>		
SEQ ID NO:4	CCAACCTCAC	CCCACAGGGC	CTCAGTCGCC	ACCATGT		

	550	560	570	580	590	600
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	GAGCATTCAC	CCATGACCGG	TCACAGCTAC	AAATCCAGAG	ACCATCAATC	CTGCTAGAGT
	CTCGTAAGGT	GGTACTGGCC	AGTGTCGATG	TTTAGGTCTC	TGGTAGTTAG	GACGATCTCA

	610	620	630	640	650	660
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	GCAGGGTGGC	AAGCACCCAA	GGGTGGCTGA	CCAAGACTGC	AGAGTCTCCT	CCATCTTCAG
	CGTCCCACCG	TTCGTGGGTT	CCCACCGACT	GGTCTGACG	TCTCAGAGGA	GGTAGAAGTC

	670	680	690	700	710	720
	* *	* *	* *	* *	* *	* *
SEQ ID NO:4	GTCCATTTCAG	CCTCCTGGCA	TTTAACTACC	AGCATCCAGT	GGTCCCCAAG	GAATCCCTTC
	CAGGTAAGTC	GGAGGACCGT	AAATGATGG	TCGTAGGTCA	CCAGGGGTTC	CTTAGGGAAG

	730	740	750	760	770	780
	*	*	*	*	*	*
SEQ ID NO:4	CTAGCCTCCT	GACATGAGTC	TGCTGGAAAG	AGCATCCAAA	CAAACAAGTA	ATAAATAAAT
	GATCGGAGGA	CTGTACTCAG	ACGACCTTTC	TCGTAGGTTT	GTTTGTTTCAT	TATTTATTTA

	790	800
	*	*
SEQ ID NO:4	AAATAAACTC	AATGCAGACA
	TTTATTTGAG	TTACGTCTGT